

GenCore version 5.1.4 p5.4578
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OM protein - protein search, using sw model

Run on: March 28, 2003, 12:02:57 ; Search time 20.2167 Seconds
(without alignments)
1550.996 Million cell updates/sec

Title: US-09-924-946-2

Perfect score: 4180

Sequence: 1 MANSPPATLFLLLGQPP.....YPANAELSLEQELRNLLI 756

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4174	99.9	756	1 L0L4_HUMAN	Q96jb6 homo sapien
2	3641.5	87.1	757	1 L0L4_MOUSE	Q924c6 mus musculus
3	2268.5	54.3	774	1 L0L2_HUMAN	Q9y4k0 homo sapien
4	2263	54.1	753	1 L0L3_HUMAN	P58215 mus musculus
5	2222	53.2	754	1 L0L3_MOUSE	Q92175 mus musculus
6	850	20.3	219	1 L0L2_MOUSE	P58022 mus musculus
7	655.5	15.7	1436	1 WC11_BOVIN	P30205 bos taurus
8	633.5	15.2	875	1 NETR_MOUSE	P56730 homo sapien
9	611.5	14.6	761	1 LYOX_RAT	Q08762 mus musculus
10	581	13.9	411	1 LYOX_CHICK	P16636 rattus norv
11	579	13.9	420	1 LYOX_MOUSE	Q05063 gallus gall
12	574.5	13.7	411	1 LYOX_HUMAN	P28301 mus musculus
13	572	13.7	417	1 L0L1_HUMAN	P28300 homo sapien
14	561.5	13.4	574	1 SPER_STRPU	Q08397 homo sapien
15	483	11.6	532	1 CD5L_MOUSE	P16264 strongyloce
16	461	11.0	347	1 CD5L_HUMAN	Q43866 homo sapien
17	445.5	10.7	352	1 CD5L_MOUSE	Q9qwk4 mus musculus
18	374	8.9	668	1 CD6_HUMAN	P30203 homo sapien
19	337.5	8.1	110	1 L0L1_MOUSE	P97873 mus musculus
20	337	8.1	665	1 CD6_MOUSE	Q61003 mus musculus
21	307.5	7.4	458	1 MSRE_MOUSE	P30204 mus musculus
22	303.5	7.3	451	1 MSRE_HUMAN	P21757 homo sapien
23	295.5	7.1	454	1 MSRE_RABIT	Q05585 oryctolagus
24	287.5	6.9	453	1 MRCO_BOVIN	P21758 bos taurus
25	255	6.1	520	1 MRCO_HUMAN	Q9uew3 homo sapien
26	250	6.0	518	1 MTCO_MOUSE	Q60754 mus musculus
27	248.5	5.9	483	1 MRCO_MESAU	Q9wb9 mesocricetu
28	155.5	3.7	1629	1 AT59_HUMAN	Q9p2n4 homo sapien
29	149.5	3.6	495	1 CD5_HUMAN	P06127 homo sapien
30	140	3.3	494	1 CD5_MOUSE	P13379 mus musculus
31	136.5	3.3	491	1 CD5_RAT	P51882 rattus norv
32	123	2.9	583	1 CFAT_HUMAN	P05156 homo sapien
33	122.5	2.9	495	1 CD5_BOVIN	P19238 bos taurus

ALIGNMENTS

RESULT 1

ID	L0L4_HUMAN	STANDARD;	PRT;	756 AA.
AC	Q96JB6; Q96PC0; Q96DY1;			
DT	15-JUN-2002 (Rel. 41, Created)			
DT	15-JUN-2002 (Rel. 41, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Lysyl oxidase homolog 4 precursor (EC 1.4.3.-) (Lysyl oxidase-like protein 4) (Lysyl oxidase related protein C).			
GN	LOXL4 OR LOXC.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Testis;			
RX	MEDLINE=21316447; PubMed=11292829;			
RA	Ito H., Akiyama H., Iguchi H., Miyamoto M., Ohsawa K., Nakamura T.;			
RT	"Molecular cloning and biological activity of a novel lysyl oxidase-related gene expressed in cartilage."			
RL	J. Biol. Chem. 276:24023-24029(2001).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=21550107; PubMed=11691589;			
RA	Maki J.M., Tikkanen H., Kivirikko K.I.;			
RT	"Cloning and characterization of a fifth human lysyl oxidase isoenzyme: the third member of the lysyl oxidase-related subfamily with four scavenger receptor cysteine-rich domains."			
RL	Matrix Biol. 20:493-496(2001).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Placenta;			
RA	Asuncion L.F., Fogelgren B., Fong K.S.K., Fong S.F.T., Kim Y., Csizsar K.;			
RT	"A novel human lysyl oxidase-like gene (LOXL4) on chromosome 10q24 has an altered SRCR domain and is down-regulated by H-ras."			
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Eye;			
RA	Strausberg R.;			
RL	Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- FUNCTION: May modulate the formation of a collagenous extracellular matrix.			
CC	-!- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTQ) (BY SIMILARITY).			
CC	-!- SUBCELLULAR LOCATION: Extracellular (potential).			
CC	-!- TISSUE SPECIFICITY: Expressed in many tissues, the highest levels among the tissues studied being in the skeletal muscle, testis and pancreas. Expressed in cartilage.			
CC	-!- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A LYSINE (BY SIMILARITY).			
CC	-!- SIMILARITY: CONTAINS 4 SRCR DOMAINS.			
CC	-!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.			

Q13753 homo sapien
Q61129 mus musculus
Q04592 mus musculus
Q07017 streptomyce
Q03610 caenorhabdi
P46531 homo sapien
Q62217 mus musculus
P98159 drosophila
P98167 bos taurus
Q90y57 brachydanio
Q9uaw3 rattus norv
Q9umf0 homo sapien

34 120 2.9 1193 1 LMG2_HUMAN
35 116 2.8 603 1 CFAT_MOUSE
36 113.5 2.7 1877 1 PKCS_MOUSE
37 113 2.7 3519 1 OLS6_STRAT
38 111 2.7 1416 1 YN81_CABEL
39 110 2.6 2556 1 NTC1_HUMAN
40 109.5 2.6 1077 1 SMSA_MOUSE
41 109.5 2.6 2616 1 NDL_DROME
42 109 2.6 867 1 SSP0_BOVIN
43 107 2.6 1242 1 JAGL_BRARE
44 106 2.5 604 1 CFAT_RAT
45 106 2.5 924 1 ICA5_HUMAN

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CC
CC EMBL; AF338441; AAK71934.1; -
CC EMBL; AY036093; AAK64186.1; -
CC EMBL; AF395336; AAL27543.1; -
CC EMBL; BC013153; AAL13153.1; -
CC Genew; HGNC:17171; LoxL4.
CC InterPro; IPR001695; Lysyl oxidase.
CC InterPro; IPR001190; Srcr_receptor.
CC Pfam; PF01186; Lysyl oxidase; 1.
CC Pfam; PF00530; SRCR; 4.
CC ProDom; PD013887; Lysyl oxidase; 1.
CC ProSITE; PS00926; LYSYL OXIDASE; FALSE_NEG.
CC ProSITE; PS00420; SRCR; 1; 1.
CC ProSITE; PS0287; SRCR; 2; 4.
CC Oxidoreductase; Copper; Glycoprotein; Repeat; Signal.
CC POTENTIAL.
CC FT SIGNAL 1 24
CC FT CHAIN 25 756
CC FT DOMAIN 32 133
CC FT DOMAIN 159 287
CC FT DOMAIN 311 411
CC FT DOMAIN 421 529
CC FT DOMAIN 533 736
CC FT METAL 611 611
CC FT METAL 613 613
CC FT METAL 615 615
CC FT MOD_RES 638 638
CC
CC MOD_RES 674 674
CC CARBOHYD 198 198
CC CARBOHYD 629 629
CC CONFLICT 3 3
CC CONFLICT 101 101
CC CONFLICT 405 405
CC CONFLICT 493 493
CC CONFLICT 539 539
CC CONFLICT 542 542
CC CONFLICT 703 703
CC SEQUENCE 756 AA; 84483 MW; 13051ACADB922BBC CRC64;
CC
CC Query Match 99.9%; Score 4174; DB 1; Length 756;
CC Best Local Similarity 99.9%; Pred. No. 0;
CC Matches 755; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
CC
CC 1 MAWSPATLFLFLLGPPSPRPSQSLGTTKRLVGPSPKPEGRLEVLHQGWGTVCCD 60
CC 1 MAWSPATLFLFLLGPPSPRPSQSLGTTKRLVGPSPKPEGRLEVLHQGWGTVCCD 60
CC
CC 61 NFAIQEATVACRQLGFEAALTAHSAKYGQEGPIWLVNRCVGTESLDQCGSGNGVS 120
CC 61 NFAIQEATVACRQLGFEAALTAHSAKYGQEGPIWLVNRCVGTESLDQCGSGNGVS 120
CC
CC 121 DCSHSDGVVTCPRRHRYGLSETVSNALGPGRRLEEVRLKPIILASAKQSPVTEGAVE 180
CC 121 DCSHSDGVVTCPRRHRYGLSETVSNALGPGRRLEEVRLKPIILASAKQSPVTEGAVE 180
CC
CC 181 VKYEGHRVQCDGWTMNSRWVCMGLFPSEVPVDSHYRYKRWOLKMRDPKSLKLTN 240
CC 181 VKYEGHRVQCDGWTMNSRWVCMGLFPSEVPVDSHYRYKRWOLKMRDPKSLKLTN 240
CC
CC 241 KNSFWIHQVTCGTGPHMANCOVAPARGKLRPCPGGMHVAVSCVAGPHFRPPKTKPQ 300
CC 241 KNSFWIHQVTCGTGPHMANCOVAPARGKLRPCPGGMHVAVSCVAGPHFRPPKTKPQ 300
CC
CC 301 RKGSWAEPVRLRSQAQVGEGRVLMNRQMGTVCDHRNKLISASVVCRLQFGFSAREA 360

DB 301 RKGSWAEPVRLRSQAQVGEGRVLMNRQMGTVCDHRNKLISASVVCRLQFGFSAREA 360
QY 361 LFGARLQGGIPIHLSEVRCRGYERTLSDCPALGSGNCGCHENAAAVRCNVPNMGFQ 420
DB 361 LFGARLQGGIPIHLSEVRCRGYERTLSDCPALGSGNCGCHENAAAVRCNVPNMGFQ 420
QY 421 VRLAGRIPEEGLEVEQVGVNPGVSGVSENKGLTEANVACRQLGLGFALHAYKETWF 480
DB 421 VRLAGRIPEEGLEVEQVGVNPGVSGVSENKGLTEANVACRQLGLGFALHAYKETWF 480
QY 481 WSGTPRAQEVVMSGVRCSGTETALQCCQRHGPVHCCHGK RFLAGVSCMSAPDLVMAQ 540
DB 481 WSGTPRAQEVVMSGVRCSGTETALQCCQRHGPVHCCHGK RFLAGVSCMSAPDLVMAQ 540
QY 541 LVQETAYLEDRPLSOLYCAHEENCLSKSADHMDPYPYRI LLRFSTQIYNLGRDTPRKT 600
DB 541 LVQETAYLEDRPLSOLYCAHEENCLSKSADHMDPYPYRI LLRFSTQIYNLGRDTPRKT 600
QY 601 GRDSVWHQCHRHVHSIEVTHYDILLTSLNGSKVAEGHKA:FCLEDTNCTGLORRYACAN 660
DB 601 GRDSVWHQCHRHVHSIEVTHYDILLTSLNGSKVAEGHKA:FCLEDTNCTGLORRYACAN 660
QY 661 FGEQGVTVGQMDTYRHDI DCQWVDITDVGPNYIFQVIVNPHYVEVAESDFSNMLQCRCK 720
DB 661 FGEQGVTVGQMDTYRHDI DCQWVDITDVGPNYIFQVIVNPHYVEVAESDFSNMLQCRCK 720
QY 721 YDGRVWLHNCHTGNSYPANAELSLEQORLRNNLI 755
DB 721 YDGRVWLHNCHTGNSYPANAELSLEQORLRNNLI 755
RESULT 2
LOLA MOUSE STANDARD; PRT; 757 AA.
AC Q924C6;
DT 15-JUN-2002 (Rel. 41, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DE Lysyl oxidase homolog 4 precursor (EC 1.4.3.-) (Lysyl oxidase-like protein 4) (lysyl oxidase related protein C).
GN LoxL4 OR LOXC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21316447; PubMed=11292829;
RA Ito H., Akiyama H., Iguchi H., Iyama K., Miyamoto M., Ohsawa K., Nakamura T.;
RT "Molecular cloning and biological activity of a novel lysyl oxidase-related gene expressed in cartilage."
RL J. Biol. Chem. 276:24023-24029(2001).
CC -!- FUNCTION: May modulate the formation of a collagenous extracellular matrix.
CC -!- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTO) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Extracellular (potential).
CC -!- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF A TYROSYL RESIDUE CROSSLINKED TO THE EPILON-AMINO GROUP OF A LYSINE (BY SIMILARITY).
CC -!- SIMILARITY: CONTAINS 4 SRCR DOMAINS.
CC -!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
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CC EMBL; AF338440; AAK71933.1; -
CC MGD; MGI:1914823; LoxL4.
DR

DR InterPro; IPR001695; Lysyl oxidase.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF01186; Lysyl oxidase; 1.
DR Pfam; PF00530; SRCR_4.
DR PRODOM; PD013887; Lysyl oxidase; 1.
DR PROSITE; PS00926; LYSYL OXIDASE; FALSE_NEG.
DR PROSITE; PS00420; SRCR_1; 1.
DR PROSITE; PS0287; SRCR_2; 4.
KM Oxidoreductase; Copper; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 25
FT CHAIN 26 757
FT DOMAIN 33 134
FT DOMAIN 160 288
FT DOMAIN 312 412
FT DOMAIN 422 530
FT DOMAIN 534 737
FT METAL 612 612
FT METAL 614 614
FT METAL 616 616
FT MOD_RES 639 639
FT MOD_RES 675 675
FT CARBOHYD 199 199
FT CARBOHYD 615 615
FT CARBOHYD 630 630
SQ SEQUENCE 757 AA; 84705 MW; D9861368F63B7B2A CRC64;
Query Match 87.1%; Score 3641.5; DB 1; Length 757;
Best Local Similarity 86.4%; Pred. No. 8.5e-279;
Matches 654; Conservative 43; Mismatches 59; Indels 1; Gaps 1;
QY 1 MAWSPATLFLF LLLGGPPPPRPSQGLTKRLVGPESKPERGRLEVLHQQGWTGCD 59
DB 1 MWWQPPTFSLFLLLLLSQAFSSRPSQSGTKRLVGPADRPBEGRLLEVLHQQGWTGCD 60
QY 60 DNFAIOEATVACQLGFEBALTAHSAKYQGGEGPIWLDNVRVCVTGTESSLDQCSNGWGV 119
DB 61 DDFALQEAATVACQLGFESALTWAHSAKYQGGEGPIWLDNVRVCIGTGLTQCSNGWGI 120
QY 120 SDCSHSDGVLCPRHRGYLSETVSNALGPQRRLEEVRLKPLASAKHSPVTEGAV 179
DB 121 SDCRESDGVVCHPRQGHYSEKVSNAIGPQRRLEEVRLKPLASAKHSPVTEGAV 180
QY 180 EVKYEGHVRQVCDQGTMMNSRVVCGMLGFPSEVPDHYVYKRWDLKMRDPKSLKSLT 239
DB 181 EVRYDGHVRQVCDQGTMMNSRVVCGMLGFPSTQSVNSHYRKWNLLKMKDPKSLNLT 240
QY 240 NKNSEFWIHVTCGLTEPHMANQVAPARGKLRPACPGGMHVVSCVAGPHFRPKTKP 299
DB 241 KKNSEFWIHVRDCEGTEPHLAKQVQVAPRGKLRPACPGGMHVVSCVAGPHFRPKPKP 300
QY 300 QRKGSWAEFRVRLRSGAQVGEGRVEVLMNRQWGTVCDDRWNLLISASVVCRLGFGSARE 359
DB 301 TRKESHAELKVLRLRSGAQVGEGRVEVLMNRQWGTVCDDRWNLLISASVVCRLGFGSARE 360
QY 360 ALFGARLQGLGPIHLSVRCRGYERTLSDCPALGSGQNGCHENAAVNCVPMNGQN 419
DB 361 ALFGALQGLGPIHLSVRCRGYERTLSDCPALGSGQNGCHENAAVNCVPMNGQN 420
QY 420 QVRLAGGRIPPEGLLEQVEVGVPRAGSVCSNMGLEAMVACRQLGLGFALHAYKETW 479
DB 421 KVLRLAGGRNSEGVVEVGVPRAGSVCSNMGLEAMVACRQLGLGFALHAYKETW 480
QY 480 FWSGTGPRAGVMSVGRCSSTELALQCCQRHGPVHCSSGGGRFLAGVSCMDSAPDLVMA 539
DB 481 YWQGTPEAKEVMSVGRCSSTELALQCCQRHGPVHCSSGGGRFLAGVSCMDSAPDLVMA 540
QY 540 QLVQETAYLLEDRPLSQYCAHEENCLSKSDHMDWPYGYRLLRFRSTQYINLGRDTRPK 599
DB 541 QLVQETAYLLEDRPLSMYCAHEENCLSKSDHMDWPYGYRLLRFRSSQIYNLGRADFRPK 600
QY 600 TGRDSVWVHQCCHRHHSIEVFTHYDLLTLNKGSKVAEGHKASFCLEDTNCPGLQRRYACA 659

DB 601 AGRHSWIWHQCCHRHHSIEVFTHYDLLTLNKGSKVAEGHKASFCLEDTNCPGVQRRYACA 660
QY 660 NFGEQGVTVGCWDTYRHDIDCQWVDITDVGPNVIFQVIVNPHYVEVAESDFSNMQLQCRC 719
DB 661 NFGEQGVAVGCWDTYRHDIDCQWVDITDVGPDVIFQVIVNPHYVEVAESDFSNMQLQCRC 720
QY 720 KYDGHVWVHLNCHTGNISYPANAELSLEQEQRLNNLI 756
DB 721 KYDQVRVWHLNCHTGDYSYRANAELSLEQEQRLNNLI 757

RESULT 3

LOL2 HUMAN STANDARD; PRT; 774 AA.
AC Q9Y4K0; Q9Y5Y8; Q9BW70;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Lysyl oxidase homolog 2 precursor (EC 1.4.3.-) (Lysyl oxidase-like protein 2) (Lysyl oxidase related protein 2) (Lysyl oxidase-related protein WS9-14).
DE protein WS9-14).
GN LOXL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID:9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-97236759; PubMed=9079631;
RA Saito H., Papaconstantinou J., Sato H., Goldstein S.;
RT "Regulation of a novel gene encoding a lysyl oxidase-related protein in cellular adhesion and senescence.";
RL J. Biol. Chem. 272:8157-8160(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 202-774 FROM N.A.
RC TISSUE=Spleen, and Placenta;
RX MEDLINE-99230328; PubMed=10212285;
RA Jourdan-Le Saux C., Tronecker H., Bogic L., Bryant-Greenwood G.D., Boyd C.D., Csizsar K.;
RT "The LOXL2 gene encodes a new lysyl oxidase-like protein and is expressed at high levels in reproductive tissues.";
RL J. Biol. Chem. 274:12939-12944(1999).
CC -!- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTQ) (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Extracellular (potential).
CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES. HIGHEST EXPRESSION IN REPRODUCTIVE TISSUES, PLACENTA, UTERUS AND PROSTATE.
CC -!- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A LYSINE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
CC -!- SIMILARITY: CONTAINS 4 SRCR DOMAINS.
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DR EMBL; U89942; AAB49697.1; -.
DR EMBL; BC000594; AAB00594.1; -.
DR EMBL; AF17949; AAB34343.1; -.
DR Genbank; HGNC:6666; LOXL2.
DR MIM; 606663; -.
DR InterPro; IPR001695; Lysyl oxidase.
DR InterPro; IPR001190; Srcr_receptor.
DR Pfam; PF00530; SRCR; 4.

Pfam: PF01186; Lysyl oxidase; 1.
 PRINTS; PR00074; LYSYLOXIDASE.
 PRINTS; PR00258; SPBRACRTPR.
 ProDom; PD013887; Lysyl_oxidase; 1.
 SMART; SM00202; SR; 4.
 PROSITE; PS00926; LYSYL_OXIDASE; 1.
 PROSITE; PS00420; SRCR_1; 1.
 PROSITE; PS0287; SRCR_2; 4.
 Oxidoreductase; Copper; Glycoprotein; Repeat; Signal.
 T SIGNAL 1 25
 T CHAIN 26 774
 T DOMAIN 58 159
 T DOMAIN 188 302
 T DOMAIN 326 425
 T DOMAIN 435 544
 T DOMAIN 548 751
 T METAL 626 626
 T METAL 628 628
 T METAL 630 630
 T MOD_RES 653 653
 MOD_RES 689 689
 CARBOHYD 288 288
 CARBOHYD 455 455
 CARBOHYD 644 644
 CONFLICT 295 295
 CONFLICT 570 570
 CONFLICT 652 652
 CONFLICT 746 746
 CONFLICT 774 774
 SEQUENCE 774 AA; 86724 MW; 9DF5D25D4824BCCD CRC64;
 Query Match 54.3%; Score 2268.5; DB 1; Length 774;
 Best Local Similarity 55.1%; pred. No. 9.4e-170;
 Matches 408; Conservative 119; Mismatches 190; Indels 23; Gaps 5
 QY 21 PSRPSQGLTKLRILGVDSKPEGRLEVLHOGQWCTVCDNFALQEAATVACRQLGFEEAL 80
 Db 47 PQAPANVAKIQLRUAGQKRKHSEGRVEVYDQGWCTVCDDFSIHAHVVCRELGVYEA 106
 QY 81 TWHSARYGQGEPIWLDNVRVCGTSSLDQCGSNGWVSDCSHSDGVGVICPHRHGY 140
 Db 107 SWTASSSYGKGEPIWLDNLHCTGNEATLAACTSNGWGVTDCKHTEDVGWCSDKRIPGF 166
 QY 141 -LSTVSNALGPQRRLEEVLRKPLTASAKOHSPTYTEGAVEVYKEGHWQRQVDCQWTKNN 199
 Db 167 KFDNSLNIQINLENIQVEDIRIRALLSTYRKPTPWEGVEVKEGKTKWQICDKHWTKN 226
 QY 200 SRVVCGLGFPSEVPVDSHYRYKVDLKMDRPKSLKSLTKNNSFWIHQVTLGTPEHMA 259
 Db 227 SRVVCGLGFPSEVPVDSHYRYKVDLKMDRPKSLKSLTKNNSFWIHQVTLGTPEHMA 273
 QY 260 NC-----QVQVAPARKLRPACPGMHAVVSCVAGPHERPPKTPQRKGSWAEBPRVLR 315
 Db 274 SKLGLPQVSLDPMK---NVTENGHLPVVUSVCPGVQVFPDGSFRFRKAYKPEQLVRLRG 330
 QY 316 CAQVGEGRVEVLNMRQWGTCDHRWNLI SASVVCROLGFGSAREALFGARLGGGLGIHL 375
 Db 331 GAYIGEGRAVEVLKNGEWGTCDKMDLVASVVCRELGFGSAKEAVTGSRLGGQIGIHL 390
 QY 376 SEVRCRGYERTLSDCPALEGSGNGCOHENAARVRCNVNPNNGFQVRLAGGRPIEGLLE 435
 Db 391 NEIQCTGNEKSIIDCKFNAESQ-GCNHEEDAGVRCNTPAMGLQKLRNLGRNPNYGRVE 449
 QY 436 VOVEVNGVPRWGSVCSENGLTEAMVACRQLGLGFALHAYKETWFVSGTFRACEVNVSGV 495
 Db 450 VLVERNGSLVWGVCCQNGVIEAMVVCROLGLGFASNAFOETWYHWDGVNSKNVNVSGV 509
 QY 496 RCSGTGELALQOCQRHG-PVHCSHGGRFLAGVSCMSADPLVMNAQLVQETAYLEDPLS 554
 Db 510 KRCSTELSLARHEDCFDVACPCGVGVYGVAGVCSFETAPDLVNAEMVQOTTYLEDPRMF 569

555	QY	OLYCAHECNLSKSDHMDWDPYGYRRLLRPFSTQIYNIGRTJFRPKTGDRDQWVWHQCHRHYY	614
570	DB	MLQCAMBENCLSASAAQTDPPTGYRLLRPFSSQIHNNQSGDFRPNKGRHAWIWHDCRHYY	629
615	QY	HSIEVTFHYDLLTLNGSKVAEGHKASCLEDTNCTPTGLORRYACANFGEGQVTVGCWDTY	674
630	DB	HSMEVTFHYDLLNLNGTKVAEGHKASCLEDTCEBGDIQKNVECANFGDQGITWGCWDMY	689
675	QY	RHDIDCQWVDITDVGPNYIEQVTVNPHYVAESDFSNMLQCRCKYDGHVRWUJHNCHTG	734
690	DB	RHDIDCQWVDITDVGPNYIEQVTVNPHYVAESDFSNMLQCRCKYDGHVRWUJHNCHTG	749
735	QY	NSYPANAELSLEQEQRLRN	754
750	DB	GSFSEBETKEKPFHFSGLNN	769

RESULT 4

LOL3 HUMAN STANDARD; PRT; 753 AA.

AC P58215; Q96RS1; 16-OCT-2001 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Lysyl oxidase homolog 3 precursor (EC 1.4.3.1) (Lysyl oxidase-like protein 3)...

GN LOXL3 OR LOXL3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

NCBI_TaxID=9606; [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=21181571; PubMed=11284725;

RA Maki J.M., Kivirikko K.I.; "Cloning and characterization of a fourth human lysyl oxidase isoenzyme." J. Biochem. J. 355;381-387(2001).

RL [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=21280915; PubMed=11386757;

RA Jourdan-Le Saux C., Tomshe A., Ujjaszar K.; "Central nervous system, uterus, heart, and leukocyte expression of the LOXL3 gene, encoding a novel lysyl oxidase-like protein." J. Genomics 74:211-218(2001).

RL [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=21233589; PubMed=11334717;

RA Huang Y., Dai J., Tang R., Zhao W., Zhou Z., Wang W., Ying K., Xie Y., Mao Y.; "Cloning and characterization of a human lysyl oxidase-like 3 gene (hLOXL3)."

RL Matrix Biol. 20:153-157(2001).

CC -!- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTO) (BY SIMILARITY)

CC -!- SUBCELLULAR LOCATION: Extracellular (Potential).

CC -!- TISSUE SPECIFICITY: EXPRESSED IN MANY TISSUES, THE HIGHEST LEVELS AMONG THE TISSUES STUDIED BEING SEEN IN THE PLACENTA, HEART, OVARY, TESTIS, SMALL INTESTINE AND SPLEEN.

CC -!- PMW: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF A TYROSINE RESIDUE CROSSLINKED TO THE EPILON-AMINO GROUP OF A LYSINE (BY SIMILARITY).

CC -!- SIMILARITY: CONTAINS 4 SRCR DOMAINS.

CC -!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.

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DR EMBL: AF282619; AAK51671.1; -;
 DR EMBL: AF311131; AAK63205.1; -;
 DR EMBL: AF284815; AAK91134.1; -;
 DR Genew: HGNC:13869; LOXL3.
 DR InterPro: IPR001695; Lysyl oxidase.
 DR InterPro: IPR001190; Srcr_receptor.
 DR Pfam: PF00530; SRCR; 4.
 DR Pfam: PF01186; Lysyl oxidase; 1.
 DR PRINTS: PR00074; LYSYLOXIDASE.
 DR PRINTS: PR00258; SPERACTRCPTR.
 DR ProDom: PD013887; Lysyl oxidase; 1.
 DR SMART: SM00202; SR; 4.
 DR PROSITE: PS00926; LYSYL OXIDASE; 1.
 DR PROSITE: PS00420; SRCR_1; 1.
 DR PROSITE: PS0287; SRCR_2; 4.
 KW Oxidoreductase; Copper; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 25 POTENTIAL.
 FT CHAIN 26 753 LYSYL OXIDASE HOMOLOG 3.
 FT DOMAIN 44 145 SRCR 1.
 FT DOMAIN 169 282 SRCR 2.
 FT DOMAIN 307 407 SRCR 3.
 FT DOMAIN 417 525 SRCR 4.
 FT DOMAIN 529 732 LYSYL-OXIDASE LIKE.
 FT METAL 607 607 COPPER (POTENTIAL).
 FT METAL 609 609 COPPER (POTENTIAL).
 FT METAL 611 611 COPPER (POTENTIAL).
 FT MOD_RES 634 634 CROSS-LINKED TO TYROSYLQUINONE (BY SIMILARITY).
 FT MOD_RES 670 670 TYROSYLQUINONE (BY SIMILARITY).
 FT CARBOHYD 111 111 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 390 390 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 481 481 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 625 625 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 159 159 E -> K (IN REF. 3).
 SQ SEQUENCE 753 AA; 83166 MW; 582C46DA25E05A69 CRC64;
 Query Match 54.1%; Score 2263; DB 1; Length 753;
 Best Local Similarity 54.5%; Pred. No. 2.5e-170;
 Matches 419; Conservative 105; Mismatches 205; Indels 40; Gaps 10;
 QY 3 WSPATLFLFL--LLGQPPPS-----RPSLGTTLRLVLGPPSPKPBEGRLVHLHQGWG 55
 DB 9 WSPWGLLLCLLSSGLSPSPGPEKKAGSQG-LRFLAGFRPKPEYGRVEIORAGEWG 67
 QY 56 TVCDNFALQEAATVACRQIGFPAALTAHSAKYQGEGPIWLDNVRVCVGTGTFESSLDQCSN 115
 DB 68 TICDDFTLQAAHILCRELGFTGTEATGTHSAKYGPGTGRWLNDLSCSGTGQSVTECASR 127
 QY 116 GWGVSCHSHSEGVVICHPRRHRYLSETVSNALGPQGRLEEVRLKPILASAKOHSPTV 175
 DB 128 GWGNSDCTHDEAGVICKQRLPGFSDSNVIEV--EHLQVEEVRIIRPAVGWRRLPLPV 185
 QY 176 EGAVEVKYEGHWRQVCDQGWMTWNSRVVCGMLFPSPVPVDSHYRYKVKMDLKMDRPKSRL 235
 DB 186 EGLVEVRLPDGWSQVCDKWSAHNSHVVCGLFPSEKRVNAAYF-----RL 232
 QY 236 KSLTNKNSFWIHQVTLCTGTEPHMANQVQVAPARGKLRLPACPGGMHVVSCVAGPHF--- 292
 DB 233 LAQRQHSFGLHGACVGTGEAHLSCLSLEFYRANDTAR--CPGGPAAVSCVPGPVYAA 290
 QY 293 ----RPPKTPQKSGSWABEPRVRLSRGAQVGEGRVLMNRQWGTVCDDHWNLSISAVV 348
 DB 291 SGQKKQKQSKPQ-----GEARVRLKGAHPGEGRVVLKASTGTGTCRDKWDLHAASW 344
 QY 349 CROLFGSAREALFGARLGGGLPIHLSEVRCRGYETLSDCPALEGSONGCOHENAAY 408
 DB 345 CRELFGSAREALSGARMQGMGAHLSEVRCSGQELSLMKCPKHNTIAEDCSHQDAGV 404
 QY 409 RCNVNMGFQNVRLAGGRIPERGLLEEVQVGVNVPWGSVCSENWGLTEAMVACRQLGL 468
 DB 405 RCNLPYTGAETIRLSGGRSQHEGRVEVQIGGPGPLRWGLICGDDWGLEAWACRQLGL 464

QY 469 GFPAIHAYKETWFSWGTTPRAQEVVMVSGVRCSTELALQOCORHGP-VHCSHGGRFLAGVS 527
 DB 465 GVAHGLQETWYWD-SGNITEVVMVSGVRCSTELSLDQCAHHGTHITCKRTGTRFTAGVI 523
 QY 528 CWDSPADLVWNAQLVQETAYLEDRPLSQLYCAHENCLSKADHMDWPGYGRLLRFSIQ 587
 DB 524 CSBTASDLILHSALVQETAYIEDRPLHMLYCAAEENCLASARSANWPGYGRLLRFSIQ 583
 QY 588 IYNLGTDFRPKTRGRDSVWVHCHRHVHSIEVFHYDYLTLGLNGSKVAEGHKASFCLEDTN 647
 DB 584 IHNLRADFRPKAGRHVSWVHCHGHYSMDIFHYDILTNGTKVAEGHKASFCLEDTE 643
 QY 648 CPTGLQRRYACANFGEGQVTVGVGMDTYRHDIDCQWVDITDVGFGNYIFQVIVNPHYEVAE 707
 DB 644 CQEDSVSRKVECANFGEGQITVGVGMDLYRHDIDCQWIDITDVKFGNYILQVINPNEVAE 703
 QY 708 SDFSNMQLQRCYKDGHRVWLHNCHTGNSYPANAELSLEQORLNNLI 756
 DB 704 SDFTNAMKCNCKYDGHRIWVHNCHIGDAFSEANRRFRERYPGQTSNQI 752
 RESULT 5
 LOL3 MOUSE
 ID LOL3 MOUSE STANDARD; PRT; 754 AA.
 AC Q9Z175; Q9JU39;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DE Lysyl oxidase homolog 3 precursor (EC 1.4.3.-) (Lysyl oxidase-like protein 3) (Lysyl oxidase related protein 2).
 GN LOXL3 OR LOR2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J, and 129/SvJ; TISSUE=Muscle;
 RX MEDLINE=99126643; PubMed=9927484;
 RA Jang W., Hua A., Spilson S.V., Miller W., Roe B.A., Meisler M.H.;
 RT "Comparative sequence of human and mouse BAC clones from the mnd2 region of chromosome 2p13.";
 RL Genome Res. 9:53-61 (1999).
 CC -!- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTO) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Extracellular (Potential).
 CC -!- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A LYSINE (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
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 DR EMBL: AF053368; AAC83205.1; -;
 DR EMBL: AF084363; AAC95338.1; -;
 DR MGI: MGI:1337004; Lox13.
 DR InterPro: IPR001695; Lysyl oxidase.
 DR InterPro: IPR001190; Srcr_receptor.
 DR Pfam: PF00530; SRCR; 4.
 DR Pfam: PF01186; Lysyl oxidase; 1.
 DR PRINTS: PR00074; LYSYLOXIDASE.
 DR PRINTS: PR00258; SPERACTRCPTR.
 DR ProDom: PD013887; Lysyl oxidase; 1.
 DR SMART: SM00202; SR; 4.
 DR PROSITE: PS00926; LYSYL OXIDASE; 1.
 DR PROSITE: PS00420; SRCR_1; 1.
 DR PROSITE: PS0287; SRCR_2; 4.

63 HAWIWDCHRHYSMEVFTYYDLLSLNGTKVAEGHKAFCLEDETECGDIQKSYECANFG 122

Db 649 VSKRYECANFGEQGITVGCWDLYRHDIDCQWIDITDVKPGNYILQVWINPNFEVASEDFT 708

QY 663 EQGVTVGCMWYRHDIDCWVJDTVPQNYIFQVIVNPHYVEAESFNNMLQCRCKYD 722
Db 123 EQGITMGCMWYRHDIDCWVJDTVPQNYIFQVIVNPHYVEAESFNNMLQCRCKYD 182

QY 723 GHRVWLNCHTGNYPANAELSLEBQRLNN 754
Db 183 GYRIWMYCNHVGAFSETEQRFHFGSLNN 214

RESULT 7

WC11_BOVIN STANDARD; PRT: 1436 AA.
ID WC11_BOVIN STANDARD; PRT: 1436 AA.
AC P30205;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Antigen WC1.1 precursor.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93056489; PubMed=1431105;
RA Wijnjaard P.L.J., Metzelaar M.J., Machugh N.D., Morrison W.I.,
RA Clevers H.C.;
RT "Molecular characterization of the WC1 antigen expressed specifically
on bovine CD4-CD8-gamma delta T lymphocytes";
RL J. Immunol. 149:3273-3277(1992).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: CONTAINS 11 SRCR DOMAINS.

CC -----
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CC or send an email to license@isb-sib.ch).
CC -----

DR EMBL; X63723; CAA45255.1; .
DR PIR; S19913; S19913.
DR PIR; A46496; A46496.
DR InterPro; IPR001190; Srcr_receptor.
DR PRINTS; PR00258; SPERACTRCPTR.
DR SMART; SM0202; SR; 11.
DR PROSITE; PS00420; SRCR_1; 4.
DR PROSITE; PS0287; SRCR_2; 11.
KW Antigen; Repeat; Glycoprotein; Signal.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 1436 ANTIGEN WC1.1.
FT DOMAIN 28 131 SRCR 1.
FT DOMAIN 134 234 SRCR 2.
FT DOMAIN 239 340 SRCR 3.
FT DOMAIN 376 476 SRCR 4.
FT DOMAIN 481 581 SRCR 5.
FT DOMAIN 586 686 SRCR 6.
FT DOMAIN 689 789 SRCR 7.
FT DOMAIN 794 895 SRCR 8.
FT DOMAIN 931 1031 SRCR 9.
FT DOMAIN 1036 1136 SRCR 10.
FT DOMAIN 1155 1255 SRCR 11.
FT CARBOHYD 162 162 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 244 244 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 256 256 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 351 351 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 424 424 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 444 444 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 531 531 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 717 717 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 799 799 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 897 897 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 979 979 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 999 999 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1054 1054 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1086 1086 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1173 1173 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1214 1214 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1393 1393 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 1436 AA; 154196 MW; 6C72E5FDC6BA088C CRC64;

Query Match 15.7%; Score 655.5; DB 1; Length 1436;

Best Local Similarity 26.2%; Pred. No. 1.7e-43;

Matches 219; Conservative 76; Mismatches 270; Indels 271; Gaps 30;

QY 22 SRPQSLGTTKLRLVGPESKEPEGRLEVLHQQWGTVCDDNFAIQBATVACRQLGFRAALT 81

Db 366 SAPYCSDSRQLRV-DGGGFCAGRVETLDQGSWTICDDGWLDDARVVCRLGCGEALN 424

QY 82 WAHSKYGGGEGPIWLDNTRCVGTESLDDQCSGNGWSDCSHSDVDGVICHPRRHGYL 141

Db 425 ATGSAHFGAGSGPIWLDNINCTGKESHVWRCPSRGWGQHCRHKQDAGVICS----- 476

QY 142 SETVSNALGPGRRLEVRLLKPILASAKOHSPTGAVGVYEGHWRVQCDQWNNNSR 201

Db 477 -----EFLALR--MVSEDDQ--CAGMLEVFNGTGWSVCRNPMEDITVS 516

QY 202 VVCGMLGPFSEVPVDSHYKRVKMDKMRDPKSLKSLTNKNSF---WIIQVTCIGTEPHM 258

Db 517 TICRQLGCGDSGTLNS-----SVALREGFRQWVDRIQCRKTDTSL 557

QY 259 ANQOVQVAPARGKLRPACPGGMHVAVSCVAGPHFPKTKPQKGSW-AEPRVRLRSGA 317

Db 558 WQC-----PSDPNYN--SC-----SPK---EEAYIWCADSRQIRLVDDG 592

QY 318 QVGEGRVVLMMQWGTCDHRNLIISAVVCRQLGFGSAREALFGARLGGGLPHLSE 377

Db 593 GRCSGRVEILLDQSGWGICDDRWLDDARVVCRLGCGEALDATVSSFFGSGPIWLDE 652

QY 378 VRCRGVETLSDCPALGSGQNGCHENAAVRCVNPNGFQNVRLAGRIPEGLELV- 436

Db 653 VNCRGEESQVMRCPSWGRQHCNHQEDAGVICS---GF---VRLAGDGPGRVEVH 705

QY 437 ----- 436

Db 706 SGEANTPVSDGNFTLPTAQVICAEGLCKAVSVLGHMPFRESGQVWABEFCRCDGPEL 765

QY 437 -----QVEVNGVPRWGSVCSENWG 455

Db 766 WSCPRVPCPGTCLHSGAAQVVCVSYTEVQLMKNGTSQCEGQVEMKISGRWRALCASHWS 825

QY 456 LTEAMVACRQLGLGFALHAYKETWFSGTTPRAQEVVMSG-----VRCSGTELALQOC- 507

Db 826 LANANVVCRLGCGVAI-----STPRGPLHVGEGDQISTAQFHCAGSFLWSCP 875

QY 508 -QRGHPVHCWG-----GGRFLAGVSCWDSADPLVWNAOLVOETAYLEDRPLSQLY- 557

Db 876 VTALGGPDCSHGNTASVICSNGHTQVLPQCNDFLSQPAGSAASEBSSPYCSDSRQLRLVD 935

QY 558 -----CAHEENCLSKSA-----DHMDWPVGYRRL-----LRFTQIYNLGRDTPPK- 599

Db 936 GGGPCGGRVEILLDQSGWGTICDD-DWLDLDDARVVCRLGCGEALNATGSAHFGAGSGPIW 994

QY 600 -----TGRDSWVW-----HOCHRHYSIEVFTHYDLLTLNGSKVAEGHKAFCLE 644

Db 995 LDDLNTGKESHVWRCPSRGWRHDC-RHKEDAGVICS-EFLALR--MVSEDDQCGWLE 1050

QY 645 -----DTNCPTGLQ-----RRYACANPGEQVTVGCMWTVRHDIDCWVDI 685

Db 1051 VFYNGTWGVCVRSPMEDITVSVICRLCGGSGSLNTSVGLREGSRP-----RWVDL 1102

Wed Apr 2 09:14:01 2003

RESULT 8
NETR HUMAN
ID NETR HUMAN STANDARD; PRT; 875 AA.
AC P56730; Q90U16;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotysin precursor (EC 3.4.21.-) (Motopsin) (Leydin).
GN PRSS12.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA MEDLINE=98201705; PubMed=9540828;
RA Proba K., Gschwend T.P., Sonderegger P.;
RT "Cloning and sequencing of the cDNA encoding human neurotysin.";
RL Biochim. Biophys. Acta 1396:143-147(1998).
RN [2]
RN SEQUENCE OF 615-875 FROM N.A.
RC TISSUE=Testis;
RA MEDLINE=9203523; PubMed=10103056;
RA Poorafshar M., Hellman L.;
RT "Cloning and structural analysis of leydin, a novel human serine
protease expressed by the Leydig cells of the testis.";
RL Eur. J. Biochem. 261:244-250(1999).
CC 1- FUNCTION: PLAYS A ROLE IN NEURONAL PLASTICITY AND THE PROTEOLYTIC
ACTION MAY SUBSERVE STRUCTURAL REORGANIZATIONS ASSOCIATED WITH
LEARNING AND MEMORY OPERATIONS (BY SIMILARITY).
CC 2- SUBCELLULAR LOCATION: Secreted
CC 3- TISSUE SPECIFICITY: Brain and Leydig cells of the testis.
CC 4- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
CC 5- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
CC 6- SIMILARITY: CONTAINS 4 SRCR DOMAINS.
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or send an email to license@isb-sib.ch).
EMBL: AJ001531; CAA04816.1;
EMBL: AF077298; AAD25919.1;
HSSP: P00763; IDPO.
GeneW: HGNC:9477; PRSS12.
MIM: 606709;
MEROPS: S01.237;
InterPro: IPR001314; Chymotrypsin.
InterPro: IPR000001; Kringle.
InterPro: IPR001254; Ser_protease_Try.
InterPro: IPR001190; Srcr_receptor.
Pfam: PF00051; kringle_1;
Pfam: PF00085; trypsin; 1.
Pfam: PF00530; SRCR_4.
PRINTS: PR00722; CHYMOTRYPSIN.
PRINTS: PR00258; SPERACTINCFR.
ProDom: PD000395; Kringle; 1.
SMART: SM00130; KR; 1.
SMART: SM00202; SR; 4.
SMART: SM00020; Tryp_SPC; 1.
PROSITE: PS00021; KRINGLE_1; FALSE_NEG.
PROSITE: PS00070; KRINGLE_2; 1.
PROSITE: PS00420; SRCR_4; 4.
PROSITE: PS0287; SRCR_3; 3.
PROSITE: PS0240; TRYPSIN_DOM; 1.
PROSITE: PS00134; TRYPSIN_HIS; 1.
PROSITE: PS00135; TRYPSIN_SER; 1.
Hydrolase; Serine protease; Glycoprotein; Kringle; Repeat; Signal.

Query Match 15.2%; Score 633.5; D1: 1; Length 875;
Best Local Similarity 31.4%; Pred. No. 4.9e-2;
Matches 159; Conservative 54; Mismatches 69; Indels 125; Gaps 15;
QY 32 LRLVGPESKPEGRLEVLHOGQWTCDDNFAIQEATVA:ROLGFEA-ALTWAHSARYGO 90
Db 280 IRLAG-GSSVHEGRVELYHAGQWGFVCDQDDADREVI:ROLGLSGIAKAM-HQAYFGE 317
QY 91 GEGPTLIDNRCVGTSESSLDGSGNGVSDCSHSEVVG/I:CHPRRHGYLSETVSALG 150
Db 338 CSGPVLDEVRCTGNELSIQCPKSSGHEHNGHKEDAG/SCTP-----LTDGVIRLAG 391
QY 151 PQRRLLEVRLKPIASAKQHSPTVEGAVEVYEGHWRO/CDQGTMMNSRVVCGMLGFP 210
Db 392 GKGSH-----EGRLEVYRGQWGT/CDDGWTETELTYVVCROLGFK 431
QY 211 SEVPVDSHYVRKVDLKMRLDPKSLTKNSFWIHQVTCIGTETPHMANCOVQVAFARG 270
Db 432 YCKQASANIHEE-----STGPIWLDVSCSGKTRFLQCS-----RRQ 469
QY 271 KLRPACPGMHAVSVAGVPHFPPTKTPQKGSMAEER-----VRLPSGAOVGGRPV 324
Db 470 WGRHDCSHREDVSIAICPG-----CEGHRLSLGFPPVRLMDGENKKEGRV 513
QY 325 EVLMNRQWGTVDHRWNLLISASVCRQLGFGSAREALFCARLGGLGPIHLSEVRCRGE 384
Db 514 EVFINGQWGTICDDGWTDDKDAVICRGLGYKGPARTNAYFGECKGPIHVDNVKCTGNE 573
QY 385 RTLSDCPALEGSGONGCHENAAAVRGNVPMKGFQNOVRI AGGRIPETECLEEVQVEVNGVP 444
Db 574 RSLADCIKQDIGHRNCHEHSEDAGVICDY--FG-----KTAGSNKESL-----615
QY 445 RWGSGVSEWGLTEAMVACVACVACVACVACVACVACVACVACVACVACVACVACVACV 504
Db 616 --SSVC---GL--RLHRRQKRIIGKNSLRGKPMQWQ/SURLKS-----652
QY 505 QQCQRHGVHCHGGGRFLAGVSCMDS 531
Db 653 -----SHGDRULCGATILSS 668

RESULT 9
NETR MOUSE
ID NETR MOUSE STANDARD; PRT; 761 AA.
AC O09762;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Neurotysin precursor (EC 3.4.21.-) (Motopsin) (Brain-specific setim)
DE Protease 3) (BSSP-3).
GN PRSS12 OR BSSP3.

OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=97401523; PubMed=9245503;
 RA Geschwend T.P., Krueger S.R., Kozlov S.V., Wolfer D.P., Sonderegger P.;
 RT "Neurotrypsin, a novel multidomain serine protease expressed in the
 RT nervous system";
 RL Mol. Cell. Neurosci. 9:207-219(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98008848; PubMed=9344839;
 RA Yamamura Y., Yamashiro K., Tsuruoka N., Nakazato H., Tsujimura A.,
 RA Yamaguchi N.;
 RT "Molecular cloning of a novel brain-specific serine protease with a
 RT kringle-like structure and three scavenger receptor cysteine-rich
 RT motifs";
 RL Biochem. Biophys. Res. Commun. 239:386-392(1997).
 CC -1- FUNCTION: PLAYS A ROLE IN NEURONAL PLASTICITY AND THE PROTEOLYTIC
 CC ACTION MAY SUBSERVE STRUCTURAL REORGANIZATIONS ASSOCIATED WITH
 CC LEARNING AND MEMORY OPERATIONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: MOST ABUNDANT IN CEREBRAL CORTEX, HIPPOCAMPUS
 CC AND AMYGDALA.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1.
 CC -1- SIMILARITY: CONTAINS 1 KRINGLE DOMAIN.
 CC -1- SIMILARITY: CONTAINS 3 SRCR DOMAINS.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: Y13192; CAA73646.1; -;
 DR EMBL: D89871; BAA23986.1; -;
 DR HSPG; P00763; LDPO.
 DR MEROPS; S01.237; -;
 DR MGJ; MGJ.1100881; Press12.
 DR InterPro; IPR001314; Chymotrypsin.
 DR InterPro; IPR000001; Kringle.
 DR InterPro; IPR001254; Ser protease Try.
 DR InterPro; IPR001190; Srcr_receptor.
 DR Pfam; PF00051; kringle; 1.
 DR Pfam; PF00089; trypsin; 1.
 DR Pfam; PF00530; SRCR; 3.
 DR PRINTS; PR00722; CHYMOTRYPSIN.
 DR PRINTS; PR00018; KRINGLE; FALSE NEG.
 DR PRINTS; PR00258; SPERACTRCPTR.
 DR ProDom; PD000395; Kringle; 1.
 DR SMART; SM00130; KR; 1.
 DR SMART; SM00202; SR; 3.
 DR SMART; SM00020; Tryp_SPC; 1.
 DR PROSITE; PS00021; KRINGLE_1; FALSE_NEG.
 DR PROSITE; PS50070; KRINGLE_2; 1.
 DR PROSITE; PS00420; SRCR_1; 3.
 DR PROSITE; PS50287; SRCR_2; 3.
 DR PROSITE; PS50240; TRYPsin_DOM; 1.
 DR PROSITE; PS00134; TRYPsin_HIS; 1.
 DR PROSITE; PS00135; TRYPsin_SER; 1.
 KW Hydrolase; Serine protease; Glycoprotein; Kringle; Repeat; Signal.
 FT SIGNAL 1 21 POTENTIAL.
 FT CHAIN 22 761 NEUROTTRYPSIN.
 FT DOMAIN 85 157 KRINGLE.
 FT DOMAIN 166 267 SRCR 1.
 FT DOMAIN 273 373 SRCR 2.
 FT DOMAIN 386 487 SRCR 3.
 FT DOMAIN 505 761 SERINE PROTEASE.

FT DOMAIN 505 516 ZYMOGEN ACTIVATION REGION.
 FT ACT_SITE 516 517 REACTIVE BOND (POTENTIAL).
 FT ACT_SITE 562 562 CHARGE RELAY SYSTEM.
 FT ACT_SITE 612 612 CHARGE RELAY SYSTEM.
 FT ACT_SITE 711 711 CHARGE RELAY SYSTEM.
 FT DISULFID 505 636 POTENTIAL.
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 521 521 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 569 569 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 761 AA; 84118 MW; DF507B03712164E6 CRC64;
 Query Match 14.6%; Score 611.5; DB 1; Length 761;
 Best Local Similarity 29.3%; Pred. No. 2.e-40;
 Matches 165; Conservative 57; Mismatches 184; Indels 157; Gaps 17;
 QY 4 SPPTATLFLFLLILGQP-----PPSRP-----OSLGTTKRLVLG 36
 DB 114 SPAS---WAEIRGQPHNFCRSPDQSGRPFYRQAQKVDWGYCDGCGPALPVIRLVG 170
 QY 37 PESKPEGRLEVLHQGQWGTVCDDNFAIQEATVACROLGFEA-ALTWAHSAKYQGEGPI 95
 DB 171 GNS-GHEGRVELYHAGQWGTICDDQWADADVICRQLGLSGIAKAW-HQAHFGESGPI 228
 QY 96 WLDNVRCVGTPESSLDQCSNGWVSDSHSDVGVICHPRRHRGVLSETVSNALGPQGR 155
 DB 229 LLDVEVCTGNELIEQCPKSSWGBHNCHEKEDAGVSCP-----LTDGVIRLAGKSTH 282
 QY 156 LEEVRLKPILASAKQHSPTVEGAVEVYEGHWRQVCDQGWMTNNSRVVCMGLGFPSEVPV 215
 DB 283 -----EGRLEVYKGGWGTVCDDGTMTNTYVACRLLGFK----- 317
 QY 216 DSHYRKWDLKMRDPKRLKSLTNKNSFWIHQVTCLETGTEPHMANCQVQVAPARGKLRPA 275
 DB 318 ----YKQSSVNHFDGNSR-----PIWLDVSCSGKEVSFIQCS-----RQWGRHD 360
 QY 276 CPQGMHVVSCV-----AGPHRPPTKPKORKSWAEPRVRLRSQVGEGRVFLVM 328
 DB 361 CSIREVDGLTCTYPDSDGHRILSPGF-----PIRLVDGENKKEGRVEVFV 403
 QY 329 NROMGTVCDSRWNLIASVVCROLGFGSAREALFGARLQGLGPIHLSEVRCRGYERTLS 388
 DB 404 NGQWGTICDDGWTDXHAAVICROUGYKGPAPARTWAYFEGKGPIHMDNVKCTGNESKALA 463
 QY 389 DCPALEGSGNQCQCHENAAAVRCNVNPMGPFQVRLAGGRIPREGLEVEQVGVNVPWGS 448
 DB 464 DCVKQDIGRHCNHSDEAGVICD-----YLEKASSGSK---E 499
 QY 449 VCSENMGLTEAMVACROLGLGFAIHAYKETFWSGTPRAQEVYVMSGVRCSGTALQQCQ 508
 DB 500 MLSSGCGL--RLHRRQKRIIGNNSLRGAMPWQASLR----- 535
 QY 509 RHGPVHCSCGGRPLAGVSCWDS 531
 DB 536 ----LRSAHGDRLLCGATLSS 554
 RESULT 10
 LYOX RAT
 ID LYOX RAT STANDARD; PRT; 411 AA.
 AC P16636;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-lysine 6-oxidase precursor (EC 1.4.3.13) (lysyl oxidase).
 GN LOX.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP NCBI_TaxID=10116;
 RC SEQUENCE FROM N.A.
 RT TISSUE=Aorta;
 RX MEDLINE=90304121; PubMed=1973052;

RA Trackman P.C., Pratt A.M., Wolanski A., Tang S.-S., Offner G.D.,
 RA Troxler R.F., Kagan H.M.;
 RA "Cloning of rat aorta lysyl oxidase cDNA: complete codons and
 RT predicted amino acid sequence."
 RL Biochemistry 29:4863-4870(1990).
 RN [2]

RP REVISIONS.
 RX MEDLINE=91329411; PubMed=1678281;
 RA Trackman P.C., Pratt A.M., Wolanski A., Tang S.-S., Offner G.D.,
 RA Troxler R.F., Kagan H.M.;
 RT "Cloning of rat aorta lysyl oxidase cDNA: complete codons and
 RT predicted amino acid sequence."
 RL Biochemistry 30:8282-8282(1991).
 CC -!- FUNCTION: IT IS RESPONSIBLE FOR THE POSTTRANSLATIONAL OXIDATIVE
 CC DEAMINATION OF PEPTIDYL LYSINE RESIDUES IN PRECURSORS TO FIBROUS
 CC COLLAGEN AND ELASTIN.
 CC -!- CATALYTIC ACTIVITY: Peptidyl-L-lysyl-peptide + H(2)O + O(2) =
 CC peptidyl-allysyl-peptide + NH(3) + H(2)O(2). (BY SIMILARITY).
 CC -!- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTO) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- TISSUE SPECIFICITY: AORTA AND LUNG.
 CC -!- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF
 CC A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A
 CC LYSINE (BY SIMILARITY).
 CC -!- PTM: The N-terminus is blocked.
 CC -!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
 CC
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 CC
 CC EMBL; U11038; AAC52176.1; --
 CC EMBL; J02903; AAA41537.1; --
 CC PIR; A30352; A30352; Lysyl oxidase.
 CC Pfam; PF01186; Lysyl oxidase; 1.
 CC PRINTS; PR00074; LYSYLOXIDASE.
 CC ProDom; PD013887; Lysyl oxidase; 1.
 CC PROSITE; PS00926; LYSYL_OXIDASE; 1.
 CC OXIDOREDUCTASE; Copper; Signal; Glycoprotein.
 CC SIGNAL 1 21 POTENTIAL.
 CC PROPEP 22 264 POTENTIAL.
 CC CHAIN 265 411 PROTEIN-LYSINE 6-OXIDASE.
 CC DOMAIN 207 411 LYSYL-OXIDASE LIKE.
 CC METAL 286 286 COPPER (POTENTIAL).
 CC METAL 288 288 COPPER (POTENTIAL).
 CC METAL 290 290 COPPER (POTENTIAL).
 CC MOD_RES 314 314 CROSS-LINKED TO TYROSYLQUINONE (BY
 CC SIMILARITY).
 CC MOD_RES 349 349 TYROSYLQUINONE (BY SIMILARITY).
 CC CARBOHYD 91 91 N-LINKED (GLCNAC...) (POTENTIAL).
 CC CARBOHYD 138 138 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 411 AA; 46558 MW; E668C9C5AACDFC1A CRC64;

Query Match 13.9%; Score 581; DB 1; Length 411;
 Best Local Similarity 49.8%; Pred. No. 2.6e-38;
 Matches 112; Conservative 32; Mismatches 69; Indels 12; Gaps 5;

OY	509	RHGPVCHSGGGRFAGVSCMSADPLVMAQLVQETAYLEDRLPSOLYCAHENCUSKS	568
DB	192	RHRP---GYGTGYFYGL-----PDLVPDPPYVQASTYVQKMSWYNLRCAAEENCLASS	242
OY	569	ADHMO-WPYGSELLRFSTQVNLGRTDPRKTRGDSWWVHQCRRHVSJEVPTHYDILT	627
DB	243	AYRADVRDQDHRVLLRFPQRVKNQSTDFLPSRPRYSWEHSCQHVHSMDFESHYLLD	302
OY	628	LNGS-KVAEGHKASPCLEDNCTPTGLORRYACANFGQVTVGCWDTYRHIDICQWVDIT	686
DB	303	ASTQRRVAEGHKASPCLEDTSQDYGYYHRRFACHTAH-TQGLSPGCGYDTYAADICQWVDIT	361

OY 687 DVGPGNYIFQVIVNPHYEAESDFSNMQLQCRCKYDGHVWLHNC 731
 DB 362 DVQPGNYILKVSUNPSYLPESDYSNNVVRCEIRYTGHHAAVSGGC 406

RESULT 11
 LYSYL_OXIDASE
 ID LYSYL_OXIDASE STANDARD; PRT; 420 AA.
 AC Q05063; 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein-lysine 6-oxidase precursor (EC 1.4.3.13) (Lysyl oxidase).
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 OC Gallus.
 ON NCBI_TaxID=9031;
 RX MEDLINE=93077497; PubMed=1360009;
 RA Wu Y., Rich C.B., Lincecum J., Trackman P.C., Kagan H.M., Foster J.A.;
 RA "Characterization and developmental expression of chick aortic lysyl
 RT oxidase."
 RL J. Biol. Chem. 267:24199-24206(1992).
 CC -!- FUNCTION: IT IS RESPONSIBLE FOR THE POSTTRANSLATIONAL OXIDATIVE
 CC DEAMINATION OF PEPTIDYL LYSINE RESIDUES IN PRECURSORS TO FIBROUS
 CC COLLAGEN AND ELASTIN.
 CC -!- FUNCTION: IN ADDITION TO CROSS LINKING OF EXTRACELLULAR MATRIX
 CC PROTEINS, IT MAY HAVE A DIRECT ROLE IN Tumor SUPPRESSION.
 CC -!- CATALYTIC ACTIVITY: Peptidyl-L-lysyl-peptide + H(2)O + O(2) =
 CC peptidyl-allysyl-peptide + NH(3) + H(2)O(2).
 CC -!- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTO) (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- DEVELOPMENTAL STAGE: INCREASES BETWEEN DAY 8 AND 16 OF EMBRYONIC
 CC DEVELOPMENT, DURING AORTIC EMBRYOGENESIS, IN DIRECT PROPORTION
 CC TO TOTAL PROTEIN SYNTHESIS.
 CC -!- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF
 CC A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A
 CC LYSINE (BY SIMILARITY).
 CC -!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.

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 or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M97881; AAA48942.1; --
 CC PIR; A45166; A45166;
 CC InterPro; IPR001695; Lysyl oxidase.
 CC Pfam; PF01186; Lysyl oxidase; 1.
 CC PRINTS; PR00074; LYSYLOXIDASE.
 CC ProDom; PD013887; Lysyl oxidase; 1.
 CC PROSITE; PS00926; LYSYL_OXIDASE; 1.
 CC OXIDOREDUCTASE; Copper; Signal; Glycoprotein.
 CC SIGNAL 1 21 POTENTIAL.
 CC PROPEP 22 153 POTENTIAL.
 CC CHAIN 154 420 PROTEIN-LYSINE 6-OXIDASE.
 CC DOMAIN 216 420 LYSYL-OXIDASE LIKE.
 CC METAL 286 286 ARG/PRO-RICH.
 CC METAL 295 295 COPPER (POTENTIAL).
 CC METAL 297 297 COPPER (POTENTIAL).
 CC METAL 299 299 COPPER (POTENTIAL).
 CC MOD_RES 323 323 CROSS-LINKED TO TYROSYLQUINONE (BY
 CC SIMILARITY).
 CC MOD_RES 358 358 TYROSYLQUINONE (BY SIMILARITY).
 CC CARBOHYD 78 78 N-LINKED (GLCNAC...) (POTENTIAL).
 CC SEQUENCE 420 AA; 48152 MW; E0CBE81DD621F5C2 CRC64;

Query Match 13.9%; Score 579; DB 1; Length 420;
Best Local Similarity 49.8%; Pred. No. 3.9e-38;
Matches 114; Conservative 31; Mismatches 72; Indels 12; Gaps 5;

QY 505 QOCORHGVHCHGGRFLAGVSCWDSAPDLVNAQLVQETAYLEDRPLSOLYCAHEBNC 564
Db 197 RQSGRYR- --GYGTGYFYGL- ----PDLVPDPYVIOASTYVQRMVNLRCABEHC 247
QY 565 LSKSADHMD-WPYGYRRLLRFSTQIVNLGRTPKTDGRSDSWMHCHRHVHSTEVEHY 623
Db 248 LASSAYRADVRDYDNRLVLLRFPQVRVKNQGTDFLPSRPYRSHWHSCHQYHSMDEFSHY 307
QY 624 DLLTLNG-SKVAEGHKAFCLEDTNCTGLORRYACANFEGQVTVGCWDTYRHDIDCOW 682
Db 308 DLLDASSHRKVAEGHKAFCLEDTSCDYGYRYACTAH-TQGLSPCYDTYNADIDCOW 366
QY 683 VDIIDVGPNGYIFQVIVNPHYVEAFSDFNNMLQCRCKYDGHVRVWLHNC 731
Db 367 IDITDVKFGNLYKSVNPSYLVPSDYNNIVRCDIRYTGHHAYASGC 415

RESULT 12
LYOX MOUSE STANDARD; PRT; 411 AA.
AC P28301;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein-lysine 6-oxidase precursor (EC 1.4.3.13) (Lysyl oxidase)
DE (RAS excision protein).
GN LOX OR RRG.
OS Mus musculus (Mouse).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91343916; PubMed=1678898;
RA Kenyon K., Contente S., Trackman P.C., Tang J., Kagan H.M.,
RA Friedman R.M.;
RT "Lysyl oxidase and rrg messenger RNA."
RL Science 253:802-802(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=NIH Swiss;
RX MEDLINE=93300513; PubMed=8100214;
RA Contente S., Csizsar K., Kenyon K., Friedman R.M.;
RT "Structure of the mouse lysyl oxidase gene."
RL Genomics 16:395-400(1993).
CC -1- FUNCTION: IT IS RESPONSIBLE FOR THE POSTTRANSLATIONAL OXIDATIVE
CC DEAMINATION OF PEPTIDYL LYSINE RESIDUES IN PRECURSORS TO FIBROUS
CC COLLAGEN AND ELASTIN.
CC -1- FUNCTION: REGULATOR OF RAS EXPRESSION. MAY PLAY A ROLE IN TUMOR
CC SUPPRESSION.
CC -1- CATALYTIC ACTIVITY: Peptidyl-L-lysyl-peptide + H(2)O + O(2) =
CC peptidyl-allysyl-peptide + NH(3) + H(2)O(2).
CC -1- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTQ) (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Extracellular.
CC -1- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF
CC A TYROSYL RESIDUE CROSSLINKED TO THE EPSILON-AMINO GROUP OF A
CC LYSINE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.

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CC EMBL; M65142; AAA19032.1; -

DR EMBL; M65143; AAA20185.1; -;
DR EMBL; L04262; AAA99899.1; -;
DR EMBL; L04263; AAA99899.1; JOINED.
DR EMBL; L04264; AAA99899.1; JOINED.
DR MGD; MGI:96817; Lox.
DR InterPro; IPR001695; Lysyl oxidase.
DR Pfam; PF01186; Lysyl oxidase; 1.
DR PRINTS; PRO0074; LYSYLOXIDASE.
DR ProDom; PD013887; Lysyl oxidase; 1.
DR PROSITE; PS00926; LYSYL-OXIDASE; 1.
KW Oxidoreductase; Copper; Signal; Glycoprotein.
FT SIGNAL 1 21 POTENTIAL.
FT PROPEP 22 764 POTENTIAL.
FT CHAIN 265 411 PROTEIN-LYSINE 6-OXIDASE.
FT DOMAIN 207 411 LYSYL-OXIDASE LIKE.
FT METAL 286 286 COPPER (POTENTIAL).
FT METAL 288 288 COPPER (POTENTIAL).
FT METAL 290 290 COPPER (POTENTIAL).
FT MOD_RES 314 314 CROSS-LINKED TO TYROSYLQUINONE (BY
FT SIMILARITY).
FT MOD_RES 349 349 TYROSYLQUINONE (BY SIMILARITY).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 138 138 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 333 333 A -> G (IN REF. 2).
SQ SEQUENCE 411 AA; 46700 MW; DBC0563A9C0AEB52 CRC64;

Query Match 13.7%; Score 574.5; DB 1; Length 411;
Best Local Similarity 50.2%; Pred. No. 8.5e-38;
Matches 109; Conservative 32; Mismatches 67; Indels 9; Gaps 4;

QY 517 HGGGRFLAGVSCWDSAPDLVNAQLVQETAYLEDRPLSOLYCAHEBNC LSKSADHMD-WP 575
Db 197 YGTGYFYGL- ----PDLVPDPYVIOASTYVQRMVNLRCABEHC LSKSADHMD 250
QY 576 YGYRRLLRFSTQIVNLGRTPKTDGRSDSWMHCHRHVHSTEVEHYDLLTLNGS-KVA 634
Db 251 YDHRVLLRFPQVRVKNQGTDFLPSRPYRSHWHSCHQYHSMDEFSHYDLLDANTQRRVA 310
QY 635 EGHKASFCLEDTNCTGLORRYACANFEGQVTVGCWDTYRHDIDCOWVDITDVGPNYI 694
Db 311 EGHKASFCLEDTSCDYGYHRRFACTAH-TQGLSPCYDTYAADIDCOWIDITDVGPNYI 369
QY 695 FQVIVNPHYVEAFSDFNNMLQCRCKYDGHVRVWLHNC 731
Db 370 LKVSVNPSYLVPSDYNNIVRCDIRYTGHHAYASGC 406

RESULT 13
LYOX HUMAN STANDARD; PRT; 417 AA.
AC P28300;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Protein-lysine 6-oxidase precursor (EC 1.4.3.13) (Lysyl oxidase).
GN LOX.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=93024096; PubMed=1357535;
RA Mariani T.J., Trackman P.C., Kagan H.M., Eddy R.L., Shows T.B.,
RA Boyd C.D., Deak S.B.;
RT "The complete derived amino acid sequence of human lysyl oxidase and
RT assignment of the gene to chromosome 5 (extensive sequence homology
RT with the murine rrg recision gene)."
RL Matrix 12:242-248(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92128932; PubMed=1685472;

Haemaelaeninen E.R., Jones T.A., Sheer D., Taskinen K.,
 Pihlajaniemi T., Kivirikko K.I.;
 "Molecular cloning of human lysyl oxidase and assignment of the gene
 to chromosome 5q23.3-31.2";
 Genomics 11:508-516(1991).
 [3]
 SEQUENCE FROM N.A.
 MEDLINE=93318011; PubMed=10391127;
 Contente S., Kenyon K., Sriaman P., Subramanyan S., Friedman R.M.;
 "Epigenetic inhibition of lysyl oxidase transcription after
 transformation by ras oncogene";
 Mol. Cell. Biochem. 194:79-91(1999).
 [4]
 SEQUENCE OF 55-216 FROM N.A.
 TISSUE=Blood;
 MEDLINE=92332554; PubMed=1352776;
 Svinatich D.M., Twomey T.A., Macauley S.P., Krebs C.J., Yang T.P.,
 Kravetz S.A.;
 "Characterization of the human lysyl oxidase gene locus";
 J. Biol. Chem. 267:14382-14387(1992).
 [5]
 DISEASE.
 PubMed=911198;
 Khakoo A., Thomas R., Trompeter R., Duffy P., Price R., Pope F.M.;
 "Congenital cutis laxa and lysyl oxidase deficiency";
 Clin. Genet. 51:109-114(1997).
 [6]
 VARIANT GLN-158.
 MEDLINE=93300514; PubMed=8100215;
 Csizsar K., Mariani T.J., Golin J.S., Deak S.B., Boyd C.D.;
 "A restriction fragment length polymorphism results in a
 nonconservative amino acid substitution encoded within the first exon
 of the human lysyl oxidase gene";
 Genomics 16:401-406(1993).
 CC -!- FUNCTION: RESPONSIBLE FOR THE POSTTRANSLATIONAL OXIDATIVE
 DEAMINATION OF PEPTIDYL LYSINE RESIDUES IN PRECURSORS TO FIBROUS
 COLLAGEN AND ELASTIN. IN ADDITION TO CROSS-LINKING OF
 EXTRACELLULAR MATRIX PROTEINS, MAY HAVE A DIRECT ROLE IN TUMOR
 SUPPRESSION.
 CC -!- CATALYTIC ACTIVITY: Peptidyl-L-lysyl-peptide + H(2)O + O(2) =
 peptidyl-allysyl-peptide + NH(3) + H(2)O(2).
 CC -!- COFACTOR: COPPER AND LYSINE TYROSYLQUINONE (LTQ).
 CC -!- SUBCELLULAR LOCATION: Extracellular.
 CC -!- PTM: THE LYSINE-TYROSYLQUINONE IS GENERATED BY THE MODIFICATION OF A
 A TYROSYL RESIDUE CROSS-LINKED TO THE EPSILON-AMINO GROUP OF A
 LYSINE.
 CC -!- DISEASE: Deficiency in lysyl oxidase has been found in patients
 with autosomal recessive cutis laxa.
 CC -!- SIMILARITY: BELONGS TO THE LYSYL OXIDASE FAMILY.
 CC
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 CC
 EMBL; M94054; AAA59525.1; -;
 DR EMBL; S45875; AAB23549.1; -;
 DR EMBL; S78694; AAB21243.1; -;
 DR EMBL; AF030291; AAD02130.1; -;
 DR EMBL; M84150; AAA59541.1; -;
 DR PIR; S23515; S23515;
 DR PIR; A40557; A40557;
 DR Genew; HGNC:6664; LOX.
 DR MIM; 153455; -;
 DR InterPro; IPR001695; Lysyl_oxidase.
 DR Pfam; PF01186; Lysyl_oxidase; 1.
 DR PRINTS; PR000074; LYSYLOXIDASE.
 DR ProDom; PD013887; Lysyl oxidase; 1.
 DR PROSITE; PS00926; LYSYL OXIDASE; 1.
 DR OXidoreductase; Copper; Signal; Glycoprotein; Polymorphism.
 KW

FT SIGNAL 1 21
 FT PROPEP 22 770
 FT CHAIN ?1 417
 FT DOMAIN 213 417
 FT METAL 292 292
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 FT MOD_RES 320 320
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 FT CARBOHYD 81 81
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 FT VARIANT 158 158
 FT CONFLICT 102 102
 FT CONFLICT 137 137
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 FT CONFLICT 304 305
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 SQ SEQUENCE 417 AA; 46944 MW; 6412A78443E0304 CRC64;
 Query Match 13.7%; Score 572; DB 1; Length 417;
 Best Local Similarity 48.9%; Pred. No. 1.4e-17;
 Matches 110; Conservative 34; Mismatches 69; Indels 12; Gaps 5;
 QY 509 RHGPVHCCHGGRFLAGVSCMSAPDLVYNAQLVQETAYEDRPLSOLYCAHENCUSKS 568
 DB 198 RYRP---GYGTGYFOYGL-----PDLVADPYVIOASTYVQKSMYNLCRAEENCIAST 248
 QY 569 ADHMD-WPYGYRRLRFSTQIYNLGRTPRPTGRDSVWHQCHRHYSIEVFTHYDLIT 627
 DB 249 AYRADVRDVRVLLRFPORVKNQGTSDFLPSRPYSMEHSCHQHYSMDSESHYDLID 308
 QY 628 LNGS-KVAEGCHKASCLEDNCTGLQRRYACANFGEQVTVGVCWDTYRHDIQCVWDIT 686
 DB 309 ANQRRVAEGHKAAPCLEDTSQDGYHREFACTAH-TQLSPGCDYTGADIDCQWIDIT 767
 QY 687 DVGPNGYIFQVIVNPHYEAESDFSNMIOCRCKYDGHVWLHNC 731
 DB 368 DVKPGNYLLKVSVPNSVLPDESDTNNVRECDIRYTGHIAYASGC 412
 RESULT 14
 LO11 HUMAN STANDARD; PRT; 574 AA
 ID LO11 HUMAN
 AC Q08397; Q06BW7;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lysyl oxidase homolog 1 precursor (EC 1.4.3.-) (lysyl oxidase-like
 protein 1) (LOL).
 GN LOXL1 OR LOXL.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Skin fibroblast;
 RX MEDLINE=93366738; PubMed=7689553;
 RA Kenyon K., Modi W.S., Contente S., Friedman R.M.;
 RA "A novel human cDNA with a predicted protein similar to lysyl oxidase
 maps to chromosome 15q24-q25";
 RL J. Biol. Chem. 268:18435-18437(1993).
 RN [2]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Kenyon K., Sathya G., Contente S., Friedman R.M.;
 RA "Structure of the human lysyl oxidase-like gene";
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RN SEQUENCE FROM N.A.

Db 198 RGKSIKTDGHFG-----FSTGPIILDVDCGTEAHITECNMPVTP 239
QY 268 ARGKLRPACPGCMHAAVUSVAGPHFPKTKPKORKGSWAEEPRVRLRSQAQVGRGRVEVL 327
Db 240 -----YQHACPYTHNDVGVVCKPNV-----EGDIRLMDGGSPHEGRVEIM 280
QY 328 MNROWGTVDHRWNLIISASVWCRQLGFGSAREA--LFGARLGQGLGPIHLSEVRCRGYER 385
Db 281 HDDAWGTICDDGDWADANVVCRCQAGYRGAVKASGFKGEDFGFTWAPIHTSFVMCTGVED 340
QY 386 TLSDCPALEGSGONGCOHENAAAARC-----NVPNMGFQNOVRLAGGRIPBEGLEVOVE 439
Db 341 RLIDCILRDGWTWSCYHVHEDASVVCATDDDDTIEIEPKHTRVRIVG-----MGOGQGRVE 395
QY 440 VNGVPRWGSVCSENWGLTEAMVACRQLGLGFALHAYKETWFWSGTPRAQEV----- 490
Db 396 VSLGNGWRVCDPDWSDHEAKTVCYHAG-----YK--WGASRAAGSAEVSAPFDLEAP 446
QY 491 -VMSGVRCSGTE-LALQOCQR--HGPVHCSHGGGRFLAGVSCMDS-APDLVMNAQLV 542
Db 447 FIIDGITCSGVENETLSQCMKVSADMTCATGD-----VGVVCEGSTAPPSCMSIAVI 499

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